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SEQUENCE LISTING

<110> THASTRUP, Ole  
TULLIN, Soren  
POULSEN, Lars K  
BJORN, Sara P

<120> Novel Fluorescent Proteins

<130> 3759-0106P

<140> 09/619,310

<141> 2000-07-19

<150> US 08/819,612

<151> 1997-03-17

<150> PCT/DK96/00051

<151> 1996-01-31

<150> DK 1065/95

<151> 1995-09-22

<160> 23

<170> PatentIn version 3.1

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<223> GFP2 primer directed to A. victoria

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Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser		
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Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe		
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Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr		
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 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala  
 95 100 105 110

gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa 385  
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys  
 115 120 125

ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa 433  
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu  
 130 135 140

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 145 150 155

aat gga atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga 529  
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly  
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agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat 577  
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp  
 175 180 185 190

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 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala  
 195 200 205

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ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa 721  
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly  
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val  
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val  
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Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
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ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tcc gtt agt 97  
Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser  
15 20 25 30

gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt 145  
Gly Glu Gly Glu Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe  
35 40 45

att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act 193  
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr  
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act ctc tct cat ggt gtt caa tgc ttt tct aga tac cca gat cat atg 241  
Thr Leu Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met  
65 70 75

aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag 289  
Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln  
80 85 90

gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct 337  
Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala  
95 100 105 110

gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa 385  
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys  
115 120 125

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Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu  
130 135 140

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Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys  
145 150 155

aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga 529  
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly  
160 165 170

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Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp

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ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa				721												
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys																
35 40 45																
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu																
50 55 60																
Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln																
65 70 75 80																
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg																
85 90 95																
Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val																
100 105 110																
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile																
115 120 125																
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn																

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135

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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly  
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Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val  
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Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
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Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val  
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gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt 145  
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe  
35 40 45

att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act 193  
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gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys 115 120 125			385
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aat ggc atg gaa tac aat tat aac tca cat aat gta tac atc atg gca Asn Gly Met Glu Tyr Asn Ser His Asn Val Tyr Ile Met Ala 160 165 170			529
gac aaa cca aag aat ggc atc aaa gtt aac ttc aaa att aga cac aac Asp Lys Pro Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn 175 180 185 190			577
att aaa gat gga agc gtt caa tta gca gac cat tat caa caa aat act Ile Lys Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr 195 200 205			625
cca att ggc gat ggc cct gtc ctt tta cca gac aac cat tac ctg tcc Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser 210 215 220			673
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly  
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Met Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys  
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Pro Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys  
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Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile  
195 200 205

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln  
210 215 220

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu  
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gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt 145  
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35 40 45  
  
att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act 193  
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50 55 60  
  
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Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met  
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Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln  
80 85 90  
  
gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct 337  
Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala  
95 100 105 110  
  
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Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys			
145	150	155	
aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga		529	
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly			
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agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat		577	
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
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ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc		625	
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195	200	205	
ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag		673	
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu			
210	215	220	
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Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
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Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn  
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly  
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Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val  
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
195 200 205

D3  
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<213> Artificial Sequence

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